



SEQUENCE LISTING

<110> Kosan Biosciences, Inc.
Julien, Bryan

<120> TRANSFORMATION SYSTEM BASED ON THE
INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
BACTERIOPHAGE MX9

<130> 300622009940

<140> US 10/645,818

<141> 2003-08-20

<150> US 60/405,196

<151> 2002-08-21

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1647

<212> DNA

<213> Bacteriophage MX9

<400> 1

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actgcggcgg	agcggttgcc	gacgtcacca	atcgacgtca	acgctctggc	gctggagggtg	240
gcccggttg	tggccctcca	gcagcaaagt	gcgacgccgc	catcgtccgg	ccgcactttc	300
ggcgcggttg	cggatgactg	gctcatcact	gaggccaagc	gcctcgtgtg	ccccgacaat	360
gagcgccgcc	atcttcgcc	tatggaggcg	ctctggggca	tgacggatgt	ggagctcacg	420
ccgcgcgtcg	tgaaggcgca	cctggcgga	cttctcaagc	cagaggggcc	gctgagcgca	480
gccaccgtca	ataaggtgcg	ctctaccggc	aagcgcac	tcaaggcggc	gcaaatcaac	540
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gagcgccctca	cgctgacggc	agcggagtgc	cgggcgggtgc	tcccgcactt	ccgcgcggac	660
cggcgccgcg	agtttctctt	ccaggtcttt	ctggggccac	gccccggcga	agagaaggcg	720
ctcctcaagg	aagatgtgga	cgctgaggcg	cgcaccgtca	ttttccggcg	cagcaatgga	780
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cagtctggtg	gcgcgcgcc	ggagcgtcgg	tgccccgcct	gcgacaagcg	catgtggggc	1080
agtggtcgcc	ccaaaccgcg	cgtctggtac	gggctccgtc	acaccgcggc	gacactgcac	1140
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accacggacg	acgtgtacac	gcacctcgac	gaggactact	gccgcgccga	acttaacaag	1260
ttgtcgtga	aggccccgcc	gccaccacct	actcaccagg	gaggaagtga	cggcggccct	1320
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catcaccggg	cgagagcttg	ggaagctcgt	gctctaccaa	ctgagctacc	acgcgcgaac	1440
ttggccgggg	gtataccggc	gccgctgctg	agcgtcaagg	acgttgccgc	ttactctca	1500
gtgagcacgg	cgaaggtgta	ccagctcctc	gccgccggcg	tcctgcctac	cgtgtgggtg	1560
ggccagtcgc	gccgcgtcaa	gcgtgaggac	ctggacgcct	acatcgccc	cgcgacggcc	1620
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<210> 2

<211> 548

<212> PRT

<213> Bacteriophage MX9

<400> 2

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Val	Gln	Ser	Val	Ala	Ala	Gly	Pro	Arg	Ala	Thr	Pro	Trp	Gly	Val	Ser
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Ala	Ser	Trp	Tyr	Leu	Leu	Gly	Arg	Thr	Ala	Thr	Gly	Glu	Tyr	Ile	Val
		35					40					45			
Ser	Ser	Asp	Ala	Ala	Lys	Lys	Gly	His	Pro	Met	Ala	Thr	Ala	Ala	Glu
	50					55					60				
Arg	Leu	Pro	Thr	Ser	Pro	Ile	Asp	Val	Asn	Ala	Leu	Ala	Leu	Glu	Val
65					70					75					80
Ala	Arg	Leu	Val	Ala	Leu	Gln	Gln	Gln	Ser	Ala	Thr	Pro	Pro	Ser	Ser
				85					90					95	
Gly	Arg	Thr	Phe	Gly	Ala	Val	Ala	Asp	Asp	Trp	Leu	Ile	Thr	Glu	Ala
			100					105					110		
Lys	Arg	Leu	Val	Cys	Pro	Asp	Asn	Glu	Arg	Arg	His	Leu	Arg	His	Met
		115					120					125			
Glu	Ala	Leu	Trp	Gly	Met	Thr	Asp	Val	Glu	Leu	Thr	Pro	Arg	Val	Val
	130					135					140				
Lys	Ala	His	Leu	Ala	Gly	Leu	Leu	Lys	Pro	Glu	Gly	Pro	Leu	Ser	Ala
145					150					155					160
Ala	Thr	Val	Asn	Lys	Val	Arg	Ser	Thr	Gly	Lys	Arg	Ile	Ile	Lys	Ala
				165					170					175	
Ala	Gln	Ile	Asn	Gly	Glu	Trp	Gly	Pro	Val	Asn	Pro	Phe	Gly	Val	Leu
			180					185					190		
Asp	Arg	Glu	Lys	Glu	Ala	Lys	Ala	Glu	Arg	Leu	Thr	Leu	Thr	Ala	Ala
		195					200					205			
Glu	Cys	Arg	Ala	Val	Leu	Pro	His	Phe	Arg	Ala	Asp	Arg	Arg	Arg	Glu
	210					215					220				
Phe	Leu	Phe	Gln	Val	Phe	Leu	Gly	Pro	Arg	Pro	Gly	Glu	Glu	Lys	Ala
225					230					235					240
Leu	Leu	Lys	Glu	Asp	Val	Asp	Val	Glu	Ala	Arg	Thr	Val	Ile	Phe	Arg
				245					250					255	
Arg	Ser	Asn	Gly	Arg	Asp	Thr	Thr	Lys	Thr	Gly	Arg	Glu	Arg	Arg	Val
		260						265					270		
Pro	Val	Pro	Asp	Glu	Leu	Trp	Pro	Val	Leu	Leu	Asp	Ala	Met	Gln	Ala
		275					280					285			
Ser	Pro	Ser	Asp	Leu	Val	Phe	Pro	Asn	Ala	Lys	Gly	Glu	Arg	Gln	Arg
	290					295					300				
Ala	Asp	Thr	Lys	Met	Thr	Arg	Val	Leu	Arg	Thr	Ala	Leu	Ser	Ala	Ala
305					310					315					320
Gly	Val	Val	Val	Gly	Trp	Asp	Tyr	Ile	Cys	Arg	Thr	Gln	Gly	Cys	Gly
				325					330					335	
Tyr	Arg	Asp	Val	Gln	Ser	Gly	Gly	Ala	Arg	Gln	Glu	Arg	Arg	Cys	Pro
			340					345					350		
Ala	Cys	Asp	Lys	Arg	Met	Trp	Ala	Ser	Gly	Arg	Pro	Lys	Pro	Ala	Val
		355					360					365			
Trp	Tyr	Gly	Leu	Arg	His	Thr	Ala	Ala	Thr	Leu	His	Arg	Lys	Ala	Gly
	370					375					380				
Cys	Asp	Pro	Leu	Val	Ile	Lys	Leu	Val	Leu	Gly	His	Ala	Ala	Val	Asp
385					390					395					400
Thr	Thr	Asp	Asp	Val	Tyr	Thr	His	Leu	Asp	Glu	Asp	Tyr	Cys	Arg	Ala
				405					410					415	
Glu	Leu	Asn	Lys	Leu	Ser	Leu	Lys	Ala	Pro	Pro	Pro	Pro	Pro	Thr	His
			420					425					430		
Gln	Gly	Gly	Ser	Asp	Gly	Gly	Pro	Asp	Ser	Gly	Arg	Asn	Thr	Tyr	Gly
		435					440					445			
Glu	Gly	Gly	Thr	Met	His	Gly	Leu	Gly	Asp	Leu	Gln	His	His	Arg	Ala
	450					455					460				

Arg Ala Trp Glu Ala Arg Ala Leu Pro Thr Glu Leu Pro Pro Arg Asn
 465 470 475 480
 Leu Ala Gly Gly Ile Pro Ala Pro Leu Leu Ser Val Lys Asp Val Ala
 485 490 495
 Ala Ser Leu Ser Val Ser Thr Ala Lys Val Tyr Gln Leu Leu Ala Ala
 500 505 510
 Gly Val Leu Pro Thr Val Trp Val Gly Gln Ser Arg Arg Val Lys Arg
 515 520 525
 Glu Asp Leu Asp Ala Tyr Ile Ala Arg Ala Thr Ala Thr Gly Gly Lys
 530 535 540
 Arg Gly Gly Lys
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<210> 3
 <211> 360
 <212> DNA
 <213> Bacteriophage MX9

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 atgccgcctg gcttgacat agggattcga aacctcgacc ccgagcttgg gaagctcgtg 180
 ctctaccaac tgagctacca ccgcaggcga agcaggcgcc aaagtacggg ccgccctgtg 240
 gcttgctcaac gggaagtggg gtgctactcc gtctcctcga cggtgagctg gtacgagtc 300
 tggaagtggg actcgcggtt gcgcgcgtcc cggacctcga agaggtagac gcctggctcg 360

<210> 4
 <211> 360
 <212> DNA
 <213> Bacteriophage MX9

<400> 4
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 gccttcatgg gtgagcggcg gaagggattc gaacctcga ccccgagctt gggaagctcg 180
 tgctctacca actgagctac caccgcaggc gaagcagggc gcaaagtacg ggccgccctg 240
 tggcttgctca acgggaagtg aggtgctact ccgtctcctc gacggtgagc tggtagcagt 300
 cctggaagtg ggactcgcgg ttgcgcgcgt cccggacctc gaagaggtag acgcctggct 360

<210> 5
 <211> 42
 <212> DNA
 <213> Bacteriophage MX9

<400> 5
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<210> 6
 <211> 240
 <212> DNA
 <213> Bacteriophage MX9

<400> 6
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 cacgcgatgc cgcttggtt gcacataggg attcgaaacc tcgacccoga gcttggaag 120
 ctccgcctcg acccgtccag gcgttatcag ccgttcgcaa acccttactt cgccttggg 180
 attccgggcc gggggcctgt ccattccgtc cagcgggtag caggaggtct caggggggtt 240

<210> 7
 <211> 257
 <212> DNA
 <213> Bacteriophage MX9

<400> 7
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 gggaagctcg tgctctacca actgagctac caccgcggaa cttggccggg ggtataccgg 180
 cgccgctgct gagcgtcaag gacgttgcg cttcactctc agtgagcacg gcgaagggtgt 240
 accagctcct cgccgcc 257

<210> 8
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 8
 gaaggaggca ccatgcacgg 20

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 9
 ctcaactgaga gtgaagccgc 20

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 10
 cgaggtccgg gacgcgcgca 20

<210> 11
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 11
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<210> 12
 <211> 74
 <212> DNA
 <213> Myxococcus xanthus

<400> 12
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 cccuuccgcc gcuc 74

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 13
 tatcccagca accgccggag 20

<210> 14
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 14
 cagcacgggt gcagcaac 18

<210> 15
 <211> 28
 <212> DNA
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<400> 15
 cccaattggc tcagggcagc ggctcatt 28

<210> 16
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 16
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<210> 17
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 17
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<210> 18

<211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18
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<210> 19
 <211> 1047
 <212> DNA
 <213> Chrysoperla carnea (Insect)

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 ataattgatt ggtatgcaaa attcaagcgt ggtgaaatga gcacggagga cgggtgaacgc 180
 agtggacgcc cgaaagaggt ggttaccgac gaaaacatca aaaaaatcca caaaatgatt 240
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 cgtgttggtc atatcattca tcaatatttg gatatgcgga agctctgtgc aaaatgggtg 360
 ccgcgcgagc tcacatttga ccaaaaacaa caacgtgttg atgattctga gcggtgtttg 420
 cagctgttaa ctcgtaatac acccgagttt ttccgtcgat atgtgacaat ggatgaaaca 480
 tggctccatc actacactcc tgagtccaat cgacagtcgg ctgagtgagg agcgaccggt 540
 gaaccgtctc cgaagcgtgg aaagactcaa aagtcgcgtg gcaaagtaat ggctctgtgt 600
 tttttcgtat cgcattggaat aattttttatc gattatcttg agaagggaaa aaccatcaac 660
 agtgactatt atatggcggt attggagcgt ttgaaggtcg aaatcgcggc aaaacggccc 720
 catatgaaga agaaaaaagt gttgttccac caagacaacg caccgtgcca caagtcattg 780
 agaacgatgg caaaaattca tgaattgggc ttcaattgc ttccccaccc accgtattct 840
 ccagatctgg cccccagcga ctttttcttg ttctcagacc tcaaaaggat gctcgcaggg 900
 aaaaaatttg gctgcaatga agaggtgatc gccgaaactg aggcctattt tgaggcaaaa 960
 ccgaaggagt actacaaaaa tggatatcaa aaattggaag gtcgttataa tcgttgtatc 1020
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<210> 20
 <211> 348
 <212> PRT
 <213> Chrysoperla carnea (Insect)

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 20 25 30
 Asp Ser Ala Pro Gly Lys Ser Thr Ile Ile Asp Trp Tyr Ala Lys Phe
 35 40 45
 Lys Arg Gly Glu Met Ser Thr Glu Asp Gly Glu Arg Ser Gly Arg Pro
 50 55 60
 Lys Glu Val Val Thr Asp Glu Asn Ile Lys Lys Ile His Lys Met Ile
 65 70 75 80
 Leu Asn Asp Arg Lys Met Lys Leu Ile Glu Ile Ala Glu Ala Leu Lys
 85 90 95
 Ile Ser Lys Glu Arg Val Gly His Ile Ile His Gln Tyr Leu Asp Met
 100 105 110
 Arg Lys Leu Cys Ala Lys Trp Val Pro Arg Glu Leu Thr Asn Asp Gln
 115 120 125
 Lys Gln Gln Arg Val Asp Asp Ser Glu Arg Cys Leu Gln Leu Leu Thr
 130 135 140
 Arg Asn Thr Pro Glu Asn Phe Arg Arg Tyr Val Thr Met Asp Glu Thr
 145 150 155 160

Trp	Leu	His	His	Tyr	Thr	Pro	Glu	Ser	Asn	Arg	Gln	Ser	Ala	Glu	Trp
				165					170					175	
Thr	Ala	Thr	Gly	Glu	Pro	Ser	Pro	Lys	Arg	Gly	Lys	Thr	Gln	Lys	Ser
			180					185					190		
Ala	Gly	Lys	Val	Met	Ala	Ser	Val	Asn	Phe	Asp	Ala	His	Gly	Ile	Ile
		195					200					205			
Asn	Ile	Asp	Tyr	Leu	Glu	Lys	Gly	Lys	Thr	Ile	Asn	Ser	Asp	Tyr	Tyr
	210					215					220				
Met	Ala	Leu	Leu	Glu	Arg	Leu	Lys	Val	Glu	Ile	Ala	Ala	Lys	Arg	Pro
225					230					235					240
His	Met	Lys	Lys	Lys	Lys	Val	Leu	Phe	His	Gln	Asp	Asn	Ala	Pro	Cys
				245					250					255	
His	Lys	Ser	Leu	Arg	Thr	Met	Ala	Lys	Ile	His	Glu	Leu	Gly	Phe	Glu
			260					265					270		
Leu	Leu	Pro	His	Pro	Pro	Tyr	Ser	Pro	Asp	Leu	Ala	Pro	Ser	Asp	Asn
		275					280					285			
Phe	Leu	Phe	Ser	Asp	Leu	Lys	Arg	Met	Leu	Ala	Gly	Lys	Lys	Asn	Gly
	290					295					300				
Cys	Asn	Glu	Glu	Val	Ile	Ala	Glu	Thr	Glu	Ala	Tyr	Asn	Glu	Ala	Lys
305					310					315					320
Pro	Lys	Glu	Tyr	Tyr	Gln	Asn	Gly	Ile	Lys	Lys	Leu	Glu	Gly	Arg	Tyr
				325				330						335	
Asn	Arg	Cys	Ile	Ala	Leu	Glu	Gly	Asn	Tyr	Val	Glu				
			340					345							